

Automatic acquisition of cell lineage through 4D microscopy and analysis of early *C. elegans* embryogenesis

Shuichi Onami

sonami@symbio.jst.go.jp

Kitano Symbiotic Systems Project, ERATO, JST

6-31-15 Jingumae, M-31 6A, Shibuya, Tokyo 150-0001, Japan

C. elegans is the simplest multicellular organism that has been extensively studied in the molecular biology. *C. elegans* is also the most advanced multicellular organism in genomics - genome sequencing has finished and a wide variety of post genome-sequencing projects are strongly undertaken, such as genome-wide gene-knockouting by mutagenesis or RNAi, and EST and gene expression pattern analysis. Thus, a huge number of data have accumulated and are accumulating for this organism. Currently, most of those data are qualitative observations. In addition to those qualitative data, a number of quantitative data and sophisticated computer simulation techniques are necessary for the system level understanding. In this talk, I will report on the development of our automatic cell lineage extraction system.

With this system, a variety of quantitative data, such as the timing of cell divisions and x, y, z, position of nucleus at each time point, are obtained for gene-knockouting animals. I will further report on our computer simulation systems and analysis of very early period of *C. elegans* embryogenesis.